

**From:** "Kevin Olival, PhD" <olival@ecohealthalliance.org>  
**Sent:** 03/15/2017 7:57:40 AM (-07:00)  
**To:** "predict-surveillance@ucdavis.edu" <predict-surveillance@ucdavis.edu>; "Christine Kreuder Johnson" <ckjohnson@ucdavis.edu>  
**Cc:** "Catherine Machalaba" <machalaba@ecohealthalliance.org>; "William B. Karesh" <karesh@ecohealthalliance.org>; "Jonna Mazet" <jkmazet@ucdavis.edu>; [REDACTED]  
"Evan Eskew" <eskew@ecohealthalliance.org>  
**Subject:** Re: [predict-surveillance] PREDICT surveillance call March 16th, 2017 @ 10am PT/1pm ET  
**Attachments:** viral\_accumulation\_for\_surveillance.html, ATT00001.htm

Dear all,

Chris asked me to share the attached .html document with you all in advance of tomorrow's surveillance call. It's a large file (8.2MB), but you should be able to open it easily with any web browser (e.g. Google Chrome, Safari, etc).

The document summarizes preliminary analyses from the Modeling & Analytics (M&A) team to estimate viral diversity per host from global PREDICT-1 data. The first couple of plots and table are searchable and interactive, so we encourage you to play around with these before the call if you have time. On the call, Evan Eskew (PREDICT M&A team member) and I will walk you through what we've done (+ some of the caveats with these approaches), and get suggestions on how to improve these analyses to be of the most value for surveillance and the project overall. Looking forward to the call tomorrow!

Cheers,  
Kevin